

SEQUENCE LISTING

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<111> DNA EXPRESSION IN TRANSFECTED CELLS AND ADJUVANT CARRIERS  
GUT IN TRANSFECTED CELLS

<130> 1993.11.5-11.00

<140> 09/059,671

<141> 1993-07-26

<150> GB 2351421.1

<151> 1997-01-24

<150> PCT/GB93/01110

<151> 1998-01-26

<160> 6

<170> PatentIn Ver. 2.0

<210> 1

<211> 67

<212> DNA

<213> synthetic construct

<220>

<221> CDS

<222> (22)...(66)

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crapactaga gtagegtagc c ggc att gac tac aat gat gtc taa gat aag  
Gly Ser Asp Tyr Lys Asp Arg Asp Asp Lys  
1 10

gac tgc tgc tgc tgc tgc

Gly Ser Cys Arg Ala

15

<410> 2

<411> 18

<412> FRT



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His Ser: Asg Tyr Lys Asp Ala Arg Asp Lys His Ser Tyr Arg Ala

[illegible]

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Thrivastoga griseipes 2 Gly Gly Ala Val Arg Gly Ile Glu Asp 51  
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
                                       10

tgc cgc gcg c  
 Cys Arg Ala

213 synthetic construct

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Cys Arg Ala  
1 5 1

4213 - synthetic construct

ALL INFORMATION CONTAINED HEREIN IS UNCLASSIFIED

7707377073 8809171068 4031'40175 38083'17 2'40311073 007060000 12'

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[illegible]

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60

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## FIG. 9

SEQUENCE OF LINKER OLIGONUCLEOTIDES.

## a) FLAG linker:

FLAG epitope

KhoI                      NotI           Gly Ser ASP TYR LYS ASP ASP

ASP   CTA GAC TCG AGT AGC GGC CGC GGC AGC GAC TAC AAG GAC

GAC GAC

BssHII

ASP LYS Gly Ser Cys Arg Ala (SEQ ID NO: 2)

GAC AAG GGC AGC TGC CGC GCG C (SEQ ID NO: 1)

b) [gly, ser]<sub>2</sub> linker:

KhoI                      NotI           Gly Gly Gly Gly Ser Gly Gly

Gly Gly Ser

CTA GAC TCG AGT AGC GGC CGC GGA GGC GGA TAC GGA AGC GGA

GGA GGC AGC

BssHII

Cys Arg Ala (SEQ ID NO: 4)

TGC CGC GCG C (SEQ ID NO: 3)

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## FIG. 10

SEQUENCE OF TRUNCATED AND MODIFIED IL6R.

## a) FLAGdeltailIL6R

TCTAGACTCGAGTAGCCGCGCGCGGACGCACTACAAAGGACGACGCAAGGGGAGCTGCCGCGCGCTGGAGGT  
 GGCMAATGGCAGCTGACCAAGCTTCCCAAGGGGCGACCGTTACCGTGAATTTGCCCGGGGAAGGAAGCAGCAGGCAA  
 TGTACCACTTCACTGGGTGTACTCTGGCTCAAAAACAGAGAAAGGACTACCAACAGGAACACACTGGTTCTGAG  
 GGAGCTGCAGCTCAGCGACACTGGGGACTATTTATGCTCCCTGAATGATCACCTGGTGGGGACTGTGCCCTTGCT  
 GGTGGATGTTCCCCCAGAGGAGCCCAAGCTCTCTGCTTCCGGAAGAAACCCCTTTGTCAACGCCATCTGTGAGTG  
 GCGTCCGAGCAGCAGCCCTCTCTCAACCAAGGAAGGCTGTGCTGTTTGCMAAGAAAATCAACACCAACCAACGGGA  
 GAGTGAATTCAGGTGCCCTGCCAGTATTCTCAGCAGCTGAAAAGCTTCTCTGCCAGGTGGAGATCTTGAGGGG  
 TGACAAAGTATACCACTAGTGTCACTGTGGCTTGCMAACAGTGTGGGAAGCAAGTCCAGCCACAAAGGAAGCTT  
 TCACAGCTTAAAAATGGTGCAGCCGGATCCAGCTGCCAAGCTTGTGTATCAGCCATACCTGGAAAGGCGCGCTG  
 GCTCAAACTCAGCTGCAGCAGCCCTGAGACCTGGACCCGAGTTACTACTTGTGCACTTCCAGCTTCCGATACCG  
 ACCTGTATGGTCAAAAGAGTTCAAGCTTGTGCTGCCGCTGCCCAAGTACCAATGGCTCATCCATGATGCCCTT  
 GCGAGGAGTGAAGCACTGGTCCAGGTCCGTGGGAAGGAGGAGCTTGACCTTGGCCAGTGGAGTGAATGGTCCCC  
 AGAGGTCAAGGGCACTCTTGGATAGCAGAGCCGAGGACCAACCCCGGCAAGAACTCTCTGGAAACCCACACAGGT  
 CTCTGTTGAAGACTCTGCCAACCAAGGATCAGTACGAAAGTTCTACAGAAAGCAAGAGTGTCTCGCCCCAGT  
 GCAAGAACTCTCTCACTGTCCCTGCCCACTTCTGGTAGCTGGAGGAAGCTTGGCGTTTGGGTTGCTTCTCTG  
 TGTCTTCACTCTCTGAGACTCAGCGAGAAATGGAACTCAGAGGCTGAGAAAGGAAGCAAGACGACCTCTCTCTC  
 ACCCCCAAGCTATTCTTGGGCGCACTGAAGCCGACCTTCTTCTGTTCTCTCTCTCAACCCACACAGCTCTGG  
 GTCTGACAATACCTAAACCAAGCTCCCTGGGTGTCAAGGACGCAAGAGCCCTTATGACAAACAGCAACAGAGA  
 CTACTTATCCCCAGATAA (SEQ ID NO.5)

## b) [gly,ser];deltailIL6R

TCTAGACTCGAGTAGCCGCGCGCGGAGGCGGAGGAAGCGGAGGAGGAGGAGCTGCCGCGCGCTGGAGGTGCCAAA  
 TGGCAGCTGACCAAGCTTCCCAAGGGGCGACCGTTACCGTGAATTTGCCCGGGGAAGGAAGCAGCAGGCAAATGTTAC  
 CAATCACTGGGTGTACTCTGGCTCAAAAACAGAGAAAGGACTACCAACAGGAACACACTGGTTCTGAGGGACGT  
 GCAGCTCAGCGACACTGGGGACTATTTATGCTCCCTGAATGATCACCTGGTGGGGACTGTGCCCTTGCTGGTGGG  
 TGTCCCCCAGAGGAGCCCAAGCTCTCTGCTTCCGGAAGAAACCCCTTTGTCAACGCCATCTGTGAGTGGCGTCC  
 GAGCAGCAGCCCTCTCTCAACCAAGGAAGGCTGTGCTGTTTGCMAAGAAAATCAACACCAACCAACGGGAAGAGTGA  
 CTTCAGGTGCCCTGCCAGTATTCTCAGCAGCTGAAAAGCTTCTCTGCCAGGTGGAGATCTTGAGGGGTGACAA  
 AGTATACCACTAGTGTCACTGTGGCTTGCMAACAGTGTGGGAAGCAAGTCCAGCCACAAAGGAAGCTTTTACAG  
 CTTAAAAATGGTGCAGCCGGATCCAGCTGCCAAGCTTGTGTATCAGCCATACCTGGAAAGGCGCGCTGGCTCAA  
 AGTCACTGGCAGCAGCTTGAACCTGGACCCGAGTTACTACTTGTGCACTTCCAGCTTCCGATACCGACCTGT  
 ATGCTCAAAAGAGTTCAAGCTTGTGCTGCCGCTGCCCAAGTACCAATGGCTCATCCATGATGCCCTTGGAGG  
 AGTGAAGCACTGGTCCAGGTCCGTGGGAAGGAGGAGCTTGACCTTGGCCAGTGGAGTGAATGGTCCCCAGAGGT  
 CACGGGCACTCTTGGATAGCAGAGCCGAGGACCAACCCCGGCAAGAACTCTCTGGAAACCCACACAGGTCTCTGT  
 TGAAGACTCTGCCAACCAAGGATCAGTACGAAAGTTCTACAGAAAGCAAGAGTGTCTCGCCCCAGTGCMAAG  
 ATCTCTCTCACTCTCTGCCCACTTCTGTAGCTGGAGGAAGCTTGGCGTTTGGGTTGCTTCTCTGTGCTT  
 CATCACTCTGAGACTCAGCGAGAAATGGAACTCAGAGGCTGAGAAAGGAAGCAAGACGACCTCTCTCTCAACCCCC  
 ACCGTATTCTTGGGCGCACTGAAGCCGACCTTCTTCTGTTCTCTCTCTCAACCCACACAGCTCTGGGTCTGA  
 CAATACCTTAACCAAGCTCCCTGGGTGTCAAGGACGCAAGAGCCCTTATGACAAACAGCAACAGAGACTACTT  
 ATCCCCAGATAA (SEQ ID NO.6)